

Figure S9

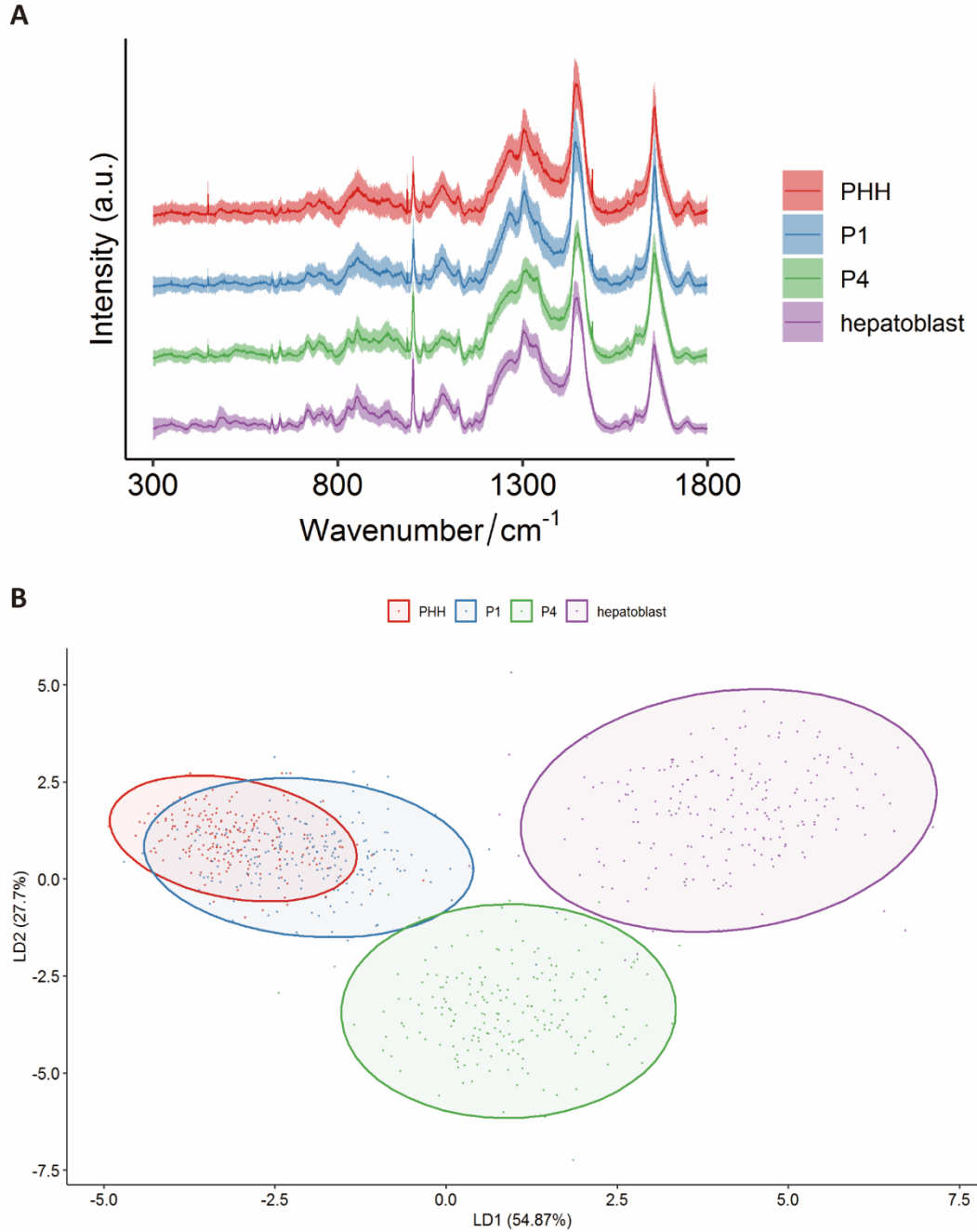


Figure S9. Raman spectroscopy and classification analysis for PHH (Lot:005), ProliHHs P1, P4 and hepatoblast. (A) The averaged spectra ($n = 815$) collected by PHH ($n = 204$), P1 ($n = 202$), P4 ($n = 202$) and hepatoblast ($n=207$) on fingerprint region. (B) Linear discriminant analysis clearly distinguished three cell groups. (The red, blue, green and purple colors represent PHH, ProliHHs P1, P4 and hepatoblast cells, respectively. PHH: primary human hepatocytes, ProliHHs: proliferating human hepatocytes, P1: passage 1, P4: passage 4)

Figure S10

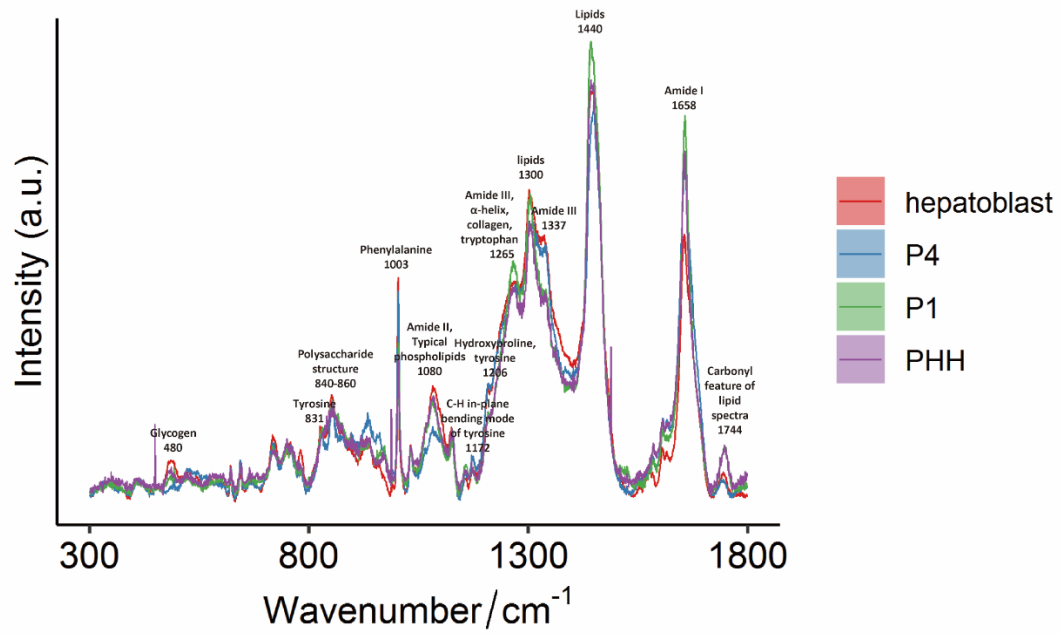


Figure S10. The biochemical molecules represented by the specific Raman bands in the average spectral (Lot:005).

Figure S11

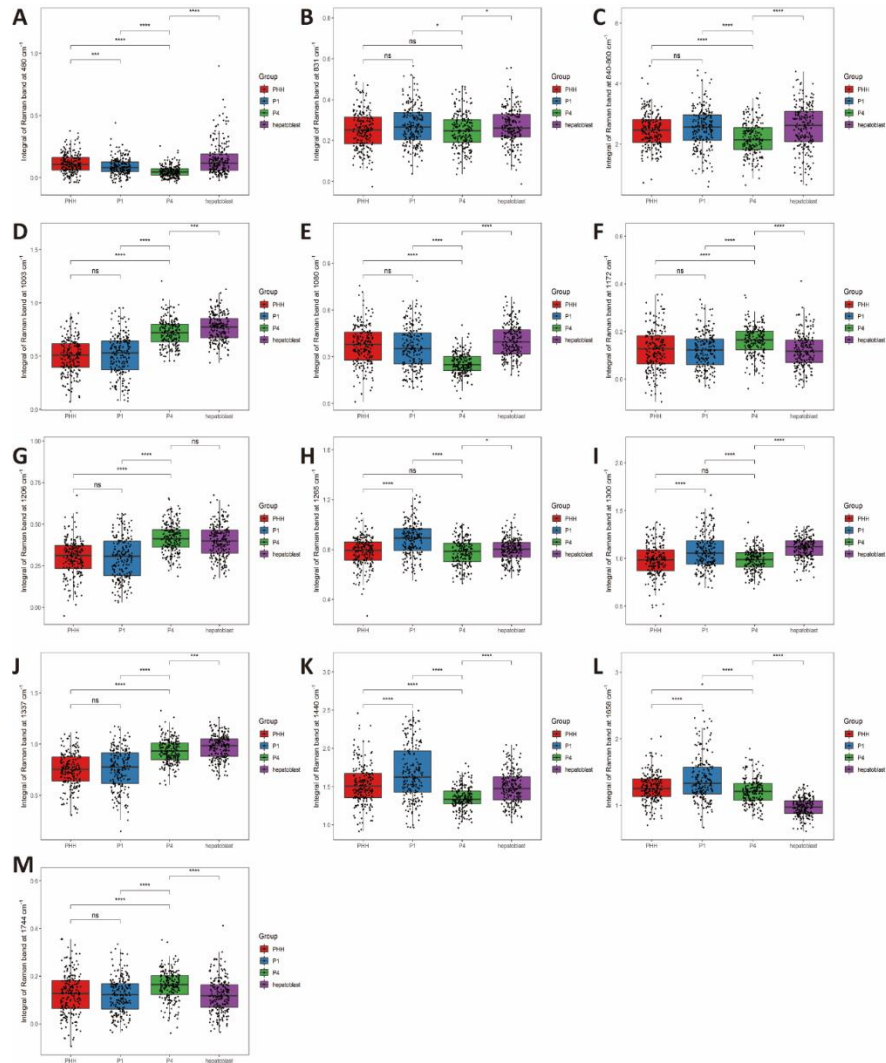


Figure S11. The peak area were semi-quantitative to compare differences of the specific Raman bands (A) 480 cm^{-1} (glycogen), (B) 831 cm^{-1} (tyrosine), (C) 840-860 cm^{-1} (polysaccharide structure), (D) 1003 cm^{-1} (phenylalanine), (E) 1080 cm^{-1} (amide II, typical phospholipid), (F) 1172 cm^{-1} (C-H in-plane bending mode of tyrosine), (G) 1206 cm^{-1} (hydroxyproline, tyrosine), (H) 1265 cm^{-1} (α -helix, collagen, tryptophan), (I) 1300 cm^{-1} (lipids), (J) 1337 cm^{-1} (amide III), (K) 1440 cm^{-1} (lipids), (L) 1658 cm^{-1} (amide I), (M) 1744 cm^{-1} (carbonyl feature of lipid spectra) in PHH (Lot:005), ProlIHs P1, P4 and hepatoblast. The results represent median, ns $P \geq 0.05$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. (PHH: primary human hepatocytes, ProlIHs: proliferating human hepatocytes, P1: passage 1, P4: passage 4)

Table S5 Machine learning by stacked (KNN, LDA, PLS, Linear-SVM, RBF-SVM, RF) model to identify cells. Overall accuracy at 92.08% (Lot: 005).

		Reference		
	hepatoblast	P1	P4	PHH
Model prediction				
hepatoblast	49	1	0	0
P1	1	45	0	7
P4	1	1	49	1
PHH	0	3	1	43
Sensitivity(%)	96.08	90	98	84.31
Specificity(%)	99.34	94.74	98.03	97.35